

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> Genes Encoding Sterol Delta-14 Reductase in Plants

<130> BB1395 PCT

<140>

<141>

<150> 60/156,820

<151> 1999-09-30

<160> 10

<170> Microsoft Office 95

<210> 1

<211> 427

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (360)

<400> 1

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cctggaaaac ttgttcctgg cgttgcaacta ctcgatggaa ctcgctctaca ctattgctgc 180
aatggctctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtc caagatgggt 240
tttgtgtctc ccaactgccat atcaaacaga ggacttgagc tgctgtccac aacttttgcc 300
ttcagttttc ttgtaaccct gatattgcat tttccgggt gcaagtcaca aagtaaaggn 360
tcatcactaa agcctcatct cagtgggaac ctgatacacg attggtgggt tgggaataca 420
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<210> 2

<211> 126

<212> PRT

<213> Glycine max

<400> 2

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Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
 1             5             10             15
Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
          20             25             30
Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
          35             40             45
Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
          50             55             60
Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
 65             70             75             80

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Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
 50 55 60
 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
 65 70 75 80
 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
 85 90 95
 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
 100 105 110
 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
 115 120 125
 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
 130 135 140
 Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
 145 150 155 160
 Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
 165 170 175
 Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
 180 185 190
 Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
 195 200 205
 Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
 210 215 220
 Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
 225 230 235 240
 Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
 245 250 255
 Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
 260 265 270
 Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
 275 280 285
 Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
 290 295 300
 Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
 305 310 315 320
 Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
 325 330 335
 Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
 340 345 350
 Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
 355 360 365

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Ile Leu Pro Tyr Val Tyr
370

<210> 5
<211> 667
<212> DNA
<213> Zea mays

<400> 5
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atctttctta ttggctacct agtgttccga ggagctaaca agcaaaaaca tgtgttcaag 120
aaggacccca aagctcctat atggggaaaaa cctcccaaag ttgtcggggg aaagctacta 180
gcatctgggt actggggcat cgcaaggcac tgcaattatc tgggagacct gctgctagca 240
ctttcgttca gcttgccctg tggagtgagt tccgtgggtc catacttcta cccacgtac 300
ctgctcattc tactggtctt gagggaaaag cgcgatgagg cgagggtgctc gcagaagtac 360
aggagatct gggcagagta ctgcaagctc gtgccgtgga ggatcctgcc ttatgtgtac 420
tgaagagacg gtagaaacca aggcagctca tggccctggg ccagctgtaa acctatttt 480
gtttgccctt aaccagttgg tgaatgttga tgtagcactc ggtaaaactgt gaccgtgcaa 540
acttttgtaa ttgttggtcc atacatgttt ggaatcgtga atcagaccgc ctacttgggt 600
ggcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
aaaaaag 667

<210> 6
<211> 140
<212> PRT
<213> Zea mays

<400> 6
Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
1 5 10 15
Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
20 25 30
Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
35 40 45
Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
50 55 60
Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
65 70 75 80
Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
85 90 95
Tyr Pro Thr Tyr Leu Leu Ile Leu Leu Val Leu Arg Glu Arg Arg Asp
100 105 110
Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
115 120 125
Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
130 135 140

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<210> 7
 <211> 1364
 <212> DNA
 <213> Glycine max

<400> 7
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 gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac tccatcttgg 120
 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 180
 cctggaaaac ttgttcctgg cgttgcaacta ctcgatggaa ctcgctctaca ctattgctgc 240
 aatgggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtgc caagatgggt 300
 tttgtgtctc ccaactgccat atcagacaga ggacttgagc tgctgtccac aacttttgcc 360
 ttcagttttc ttgtaaccct gatattgcat ttttcgggtt gcaagtcaca aagtaaaggt 420
 tcatcactaa agcctcatct cagtggaaac ctgatacacg attgggtggtt tggatatacaa 480
 ctaaattccac agttcatggg tatcgacctc aaagctggaa tgatgggatg gctacttattc 540
 aatttatcta ttcttatgaa gagcattcaa gatggtaactt tgagccagtc aatgattctc 600
 taccagctat tctgtgcact atacatcctg gactattttg tacatgaaga gtacatgaca 660
 tccacctggg acataattgc agagagactg ggcttcatgt tggcttttgg agatttagtg 720
 tggattcctt tctctttcag catacagga tgggtggtct tgatgaacag tgtggagtta 780
 acaccagctg ccattgtagc taattgcttt gtgttcctga ttggatacat ggtatttcga 840
 ggagcaaaaca agcaaaaagca tgtgttcaaa aagaatccaa aggtccttat ctggggtaag 900
 cctccaaaag tcattggtgg aaagctactt gcttctggtt attggggtat tgctagacac 960
 tgtaattacc taggggattt gatgcttgct ctctccttta gcttaccatg tgggataagt 1020
 tcaccaattc catacttcta tccaatttat cttcttattc tgtaaatctg gagagagaga 1080
 acggatgaag ctggttgctc cgagaagtat agagagatat gggccgagta tcgtaaaactt 1140
 gttccatgga gaattattgcc ttacgtttat taggatgaaa aaaaaaaggg cttcaccatg 1200
 aattcttcat cttgccgatg ttattaagca cttcgatgta aattggttct tgttcttgtg 1260
 gtttcaatct tggatctttt cttattgagc catgtagctg caggagagtg tttcgaggga 1320
 tttatcttac catctatatt tgtgtaaaaa aaaaaaaaaa aaaa 1364

<210> 8
 <211> 369
 <212> PRT
 <213> Glycine max

<400> 8
 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
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 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
 20 25 30
 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
 35 40 45
 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
 50 55 60
 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
 65 70 75 80
 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
 85 90 95
 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
 100 105 110
 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
 115 120 125

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Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
 130 135 140
 Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn
 145 150 155 160
 Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser
 165 170 175
 Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe
 180 185 190
 Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
 195 200 205
 Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
 210 215 220
 Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
 225 230 235 240
 Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
 245 250 255
 Val Phe Arg Gly Ala Asn Lys Gln Lys His Val Phe Lys Lys Asn Pro
 260 265 270
 Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val Ile Gly Gly Lys Leu
 275 280 285
 Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly
 290 295 300
 Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser
 305 310 315 320
 Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp
 325 330 335
 Arg Glu Arg Thr Asp Glu Ala Arg Cys Ala Glu Lys Tyr Arg Glu Ile
 340 345 350
 Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val
 355 360 365

Tyr
 369

<210> 9
 <211> 430
 <212> PRT
 <213> Ascobolus immersus

<400> 9
 Met Gly Gly Lys Asp Tyr Glu Phe Gly Gly Pro Ile Gly Thr Gly Val
 1 5 10 15
 Leu Met Leu Ile Leu Pro Pro Ile Ser His Tyr Leu His Phe Leu Ile
 20 25 30

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Thr Pro Arg Gly Ala Pro Pro Pro Glu Phe Trp Ser Ala Pro Leu Glu
 35 40 45
 Thr Leu Lys Ser Val Thr Pro Thr Phe Ser Ser Leu Phe Ser Leu His
 50 55 60
 Ala Thr Leu Ala Val Ala Ala Tyr Tyr Leu Leu Leu Val Ala Leu Met
 65 70 75 80
 Tyr Val Leu Pro Ala Glu Ile Ala Glu Gly Val Val Leu Lys Asp Gly
 85 90 95
 Ser Arg Leu Lys Tyr Arg Cys Asn Ala Phe Thr Thr Phe Leu Val Phe
 100 105 110
 Phe Thr Phe Leu Gly Thr Met Thr Val Leu Glu Gly Pro Thr Trp Trp
 115 120 125
 Phe Trp Ser Tyr Leu Thr Asp Asn Phe Ala Gln Leu Gln Ser Ala Ser
 130 135 140
 Ile Val Phe Ser Tyr Ala Met Ser Leu Trp Val Tyr Ile Arg Ser Tyr
 145 150 155 160
 Arg Pro Met Pro Lys Gly Lys Glu Val Ile Leu Ser Pro Val Gly Phe
 165 170 175
 Lys Gly Asn His Ile His Asp Phe Trp Met Gly Arg Glu Leu Asn Pro
 180 185 190
 Arg Ile Gly Glu Trp Leu Asp Ile Lys Gln Leu His Glu Leu Arg Pro
 195 200 205
 Gly Leu Met Gly Trp Ile Leu Phe Asn Leu Ala Trp Thr Val Lys Gln
 210 215 220
 Tyr Asn Thr His Gly Phe Val Ser Asp Ser Ile Val Leu Val Asn Leu
 225 230 235 240
 Phe Glu Thr Trp Tyr Val Val Asp Ala Leu Trp Asn Glu Ser Lys Val
 245 250 255
 Leu Thr Thr Met Asp Ile Thr Thr Asp Gly Leu Gly Val Met Leu Leu
 260 265 270
 Phe Gly Asn Ala Val Trp Val Pro Phe Met Tyr Cys Leu Gln Ala Arg
 275 280 285
 Tyr Leu Ala Ser Phe Pro Val His Leu Gly Leu Leu Gly Ile Ala Gly
 290 295 300
 Val Leu Ala Val Gln Phe Thr Gly Tyr Ala Ile Phe Arg Gly Ala Asn
 305 310 315 320
 Asn Gln Lys Asn Ala Phe Arg Thr Asn Pro Ala Asp Pro Ala Val Ser
 325 330 335
 His Leu Lys Phe Met Thr Thr Lys Ser Gly Ser Lys Leu Leu Ile Ser
 340 345 350

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Gly Trp Trp Gly Val Ala Arg His Val Asn Tyr Phe Gly Asp Trp Ile
 355 360 365

Met Ala Trp Ser Tyr Cys Leu Thr Thr Gly Phe Asn Thr Pro Leu Thr
 370 375 380

Tyr Phe Tyr Val Ile Tyr Phe Gly Ile Leu Leu Leu His Arg Asp Arg
 385 390 395 400

Arg Asp Glu Ala Lys Cys Arg Glu Lys Tyr Gly Lys Asp Trp Asp Arg
 405 410 415

Tyr Cys Lys Val Val Lys Trp Arg Ile Ile Pro Gly Ile Tyr
 420 425 430

<210> 10

<211> 365

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Asp Leu Gly Val Leu Leu Pro Ser Leu Gln Ser Val Tyr Val Leu
 1 5 10 15

Val Phe Tyr Phe Val Tyr Leu Ala Val Ala Gly Glu Ile Leu Pro Gly
 20 25 30

Lys Val Ile Arg Gly Val Leu Leu Ser Asp Gly Ser Gln Leu Arg Tyr
 35 40 45

Arg Cys Asn Gly Leu Leu Ala Leu Ile Leu Leu Val Ala Ile Leu Gly
 50 55 60

Ile Cys Ala Lys Leu Gly Ile Val Ser Pro Leu Val Val Ala Asp Arg
 65 70 75 80

Gly Leu Glu Leu Leu Ser Ala Thr Phe Ile Phe Cys Val Leu Val Thr
 85 90 95

Leu Ala Leu Tyr Val Thr Gly Arg Ser Ser Ser Asn Lys Gly Ser Ser
 100 105 110

Leu Lys Pro His Val Ser Gly Asn Leu Val His Asp Trp Trp Phe Gly
 115 120 125

Ile Gln Leu Asn Pro Gln Phe Met Ser Ile Asp Leu Lys Phe Phe Phe
 130 135 140

Val Arg Ala Gly Met Met Gly Trp Leu Leu Ile Asn Leu Ser Ile Leu
 145 150 155 160

Ala Lys Ser Val Gln Asp Gly Ser Leu Ser Gln Ser Met Ile Leu Tyr
 165 170 175

Gln Ile Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe Val His Glu Glu
 180 185 190

Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg Leu Gly Phe Met
 195 200 205
 Leu Val Phe Gly Asp Leu Leu Trp Ile Pro Phe Thr Phe Ser Ile Gln
 210 215 220
 Gly Trp Trp Leu Leu His Asn Lys Val Glu Leu Thr Val Pro Ala Ile
 225 230 235 240
 Val Val Asn Cys Leu Val Phe Leu Ile Gly Tyr Met Val Phe Arg Gly
 245 250 255
 Ala Asn Lys Gln Lys His Ile Phe Lys Lys Asn Pro Lys Thr Pro Ile
 260 265 270
 Trp Gly Lys Pro Pro Val Val Val Gly Gly Lys Leu Leu Val Ser Gly
 275 280 285
 Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Met Leu
 290 295 300
 Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser Pro Val Pro Tyr
 305 310 315 320
 Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp Arg Glu Arg Arg
 325 330 335
 Asp Glu Val Arg Cys Ala Glu Lys Tyr Lys Glu Ile Trp Ala Glu Tyr
 340 345 350
 Leu Arg Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
 355 360 365